RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/563,503A_

Source: _Hand_

Date Processed by STIC: _6/14/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
     http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/563, 503A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____ Wrapped Nucleics
Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned: Do not use tab codes between numbers; use space characters, instead.

4____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____ Variable Length — Sequence(s)____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
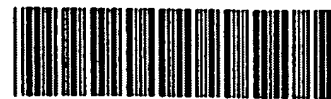
11____ Use of <220> — Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa — "n" can only represent a single underlined nucleotide; "Xaa" can only represent a single underlined amino acid

AMC – STIC Systems Branch – 03/02/06

IFWO

RAW SEQUENCE LISTING   DATE: 06/14/2006
PATENT APPLICATION: US/10/563,503A   TIME: 09:50:11   *see item 2
/ on Error Summary
Sheet*

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06142006\J563503A.raw

```
   5 <110> APPLICANT: Stordeur, Patrick
   6        Goldman, Michel
  10 <120> TITLE OF INVENTION: Device, kit and method for pulsing biological samples with
an agent and
  11        stabilising the sample so pulsed
  15 <130> FILE REFERENCE: DECLE35.005APC
  19 <140> CURRENT APPLICATION NUMBER: 10/563,503A
  20 <141> CURRENT FILING DATE: 2006-01-04
  22 <150> PRIOR APPLICATION NUMBER: PCT/EP03/07453
  23 <151> PRIOR FILING DATE: 2003-07-10
  26 <160> NUMBER OF SEQ ID NOS: 10
  28 <170> SOFTWARE: PatentIn version 3.1
  32 <210> SEQ ID NO: 1
  34 <211> LENGTH: 22
  36 <212> TYPE: DNA
  38 <213> ORGANISM: Homo sapiens
  42 <400> SEQUENCE: 1
  43 ctcaccagga tgctcacatt ta                                      22
  44 <210> SEQ ID NO: 2
  46 <211> LENGTH: 24
  48 <212> TYPE: DNA
  50 <213> ORGANISM: Homo sapiens
  54 <400> SEQUENCE: 2
  55 tccagaggtt tgagttcttc ttct                                    24
  56 <210> SEQ ID NO: 3
  58 <211> LENGTH: 25
  60 <212> TYPE: DNA
  62 <213> ORGANISM: Homo sapiens
  66 <220> FEATURE:
  68 <221> NAME/KEY: misc_feature
  70 <222> LOCATION: (1)..(1)
  72 <223> OTHER INFORMATION: N = 6Fam
  75 <220> FEATURE:
  77 <221> NAME/KEY: misc_feature
  79 <222> LOCATION: (25)..(25)
  81 <223> OTHER INFORMATION: N = Tamra-p
  84 <400> SEQUENCE: 3
W--> 85 ntgcccaaga aggccacaga actgn                                 25
  86 <210> SEQ ID NO: 4
  88 <211> LENGTH: 21
  90 <212> TYPE: DNA
  92 <213> ORGANISM: Homo sapiens
  96 <400> SEQUENCE: 4
  97 actttgaaca gcctcacaga g                                       21
```

Does Not Comply Corrected Diskette Needed

pp 1-2

"n" can only represent a nucleotide, not a label or dye.

file://C:\CRF4\Outhold\VsrJ563503A.htm   6/14/2006

BEST AVAILABLE COPY

RAW SEQUENCE LISTING   DATE: 06/14/2006
PATENT APPLICATION: US/10/563,503A   TIME: 09:50:11

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06142006\J563503A.raw

```
 98 <210> SEQ ID NO: 5
100 <211> LENGTH: 20
102 <212> TYPE: DNA
104 <213> ORGANISM: Homo sapiens
108 <400> SEQUENCE: 5
109 ttggaggcag caaagatgtc                                        20
110 <210> SEQ ID NO: 6
112 <211> LENGTH: 23
114 <212> TYPE: DNA
116 <213> ORGANISM: Homo sapiens
120 <220> FEATURE:
122 <221> NAME/KEY: misc_feature
124 <222> LOCATION: (1)..(1)
126 <223> OTHER INFORMATION: N - 6Fam
129 <220> FEATURE:
131 <221> NAME/KEY: misc_feature
133 <222> LOCATION: (23)..(23)
135 <223> OTHER INFORMATION: N = Tamra-p
138 <400> SEQUENCE: 6
139 nctgtgcacc gagttgaccg tan                                    23
140 <210> SEQ ID NO: 7
142 <211> LENGTH: 22
144 <212> TYPE: DNA
146 <213> ORGANISM: Homo sapiens
150 <400> SEQUENCE: 7
151 tgtcacaaac agtgcaccta ct                                     22
152 <210> SEQ ID NO: 8
154 <211> LENGTH: 26
156 <212> TYPE: DNA
158 <213> ORGANISM: Homo sapiens
162 <400> SEQUENCE: 8
163 agttacaata ggtagcaaac cataca                                 26
164 <210> SEQ ID NO: 9
166 <211> LENGTH: 21
168 <212> TYPE: DNA
170 <213> ORGANISM: Homo sapiens
174 <400> SEQUENCE: 9
175 taattgcctc acattgtcac t                                      21
176 <210> SEQ ID NO: 10
178 <211> LENGTH: 21
180 <212> TYPE: DNA
182 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 10
187 attcagctcg aacactttga a                                      21
```

W--> (line 139)

same error as p. 1 (handwritten annotation)

file://C:\CRF4\Outhold\VsrJ563503A.htm   6/14/2006

BEST AVAILABLE COPY

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 06/14/2006
PATENT APPLICATION: US/10/563,503A   TIME: 09:50:12

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06142006\J563503A.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 1,25
Seq#:6; N Pos. 1,23

VERIFICATION SUMMARY   DATE: 06/14/2006
PATENT APPLICATION: US/10/563,503A   TIME: 09:50:12

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06142006\J563503A.raw**

L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0